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MorphoSys AG  
Yayon, Avner  
Thomassen-Wolf, Elisabeth  
Rom, Eran  
Borges, Eric

<120> ANTIBODIES THAT BLOCK RECEPTOR PROTEIN TYROSINE KINASE ACTIVATION

<130> 81408-4400

<140> US 10/734,661  
<141> 2003-12-15

<150> US 60/299,187  
<151> 2001-06-20

<150> PCT/IL02/00494  
<151> 2002-06-20

<160> 106

<170> PatentIn version 3.2

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Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly  
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Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala  
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Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr  
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<210> 54  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VL domain

<220>  
 <221> misc\_feature  
 <222> (253)..(255)  
 <223> NNN=ACT OR GTT

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cgtttttagcg	gctctggatc	cggcactgat	tttaccctga	ccattagcag	cctgcaacct	240	
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cgtacg						306	

<210> 55  
 <211> 327  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VL domain

<400>	55						
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ggtaaagcac	cgaaactatt	aatttatgca	gccagcagct	tgcaaagcgg	ggccccgtcc	180	
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gaagactttg	cggtttatta	ttgctttcag	tatggttcta	ttcctcctac	ctttggccag	300	
ggtacgaaag	ttgaaattaa	acgtacg				327	

<210> 56  
 <211> 309  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VL domain

<220>  
 <221> misc\_feature  
 <222> (256)..(258)  
 <223> NNN=ACT OR GTT

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 ccagggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtccc 180  
 gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240  
 cctgaagact ttgcgnnnta ttattgccag acctttggcc aggggtacgaa agttgaaatt 300  
 aaacgtacg 309

<210> 57  
 <211> 330  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VL domain

<400> 57  
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 ccagggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtccc 180  
 gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240  
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 cagggtacga aagttgaaat taaacgtacg 330

<210> 58  
 <211> 330  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VL domain

<400> 58  
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 ccagggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtccc 180  
 gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240  
 cctgaagact ttgcgactta ttattgccag cagactaata atgctcctgt tacctttggc 300  
 cagggtacga aagttgaaat taaacgtacg 330

<210> 59  
 <211> 324  
 <212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 59

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attaactgca	gaagcagcca	gagcgtgctg	tatagcagca	acaacaaaaa	ctatctggcg	120
tggtaccagc	agaaaccagg	tcagccgccg	aaactattaa	tttattgggc	atccaccctg	180
gaaagcgggg	tcccggatcg	ttttagcggc	tctggatccg	gcactgattt	taccctgacc	240
atttcgtccc	tgcaagctga	agacgtggcg	gtgtattatt	gccagacctt	tggccagggt	300
acgaaagtgt	aaattaaacg	tacg				324

<210> 60

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 60

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attaactgca	gaagcagcca	gagcgtgctg	tatagcagca	acaacaaaaa	ctatctggcg	120
tggtaccagc	agaaaccagg	tcagccgccg	aaactattaa	tttattgggc	atccaccctg	180
gaaagcgggg	tcccggatcg	ttttagcggc	tctggatccg	gcactgattt	taccctgacc	240
atttcgtccc	tgcaagctga	agacgtggcg	gtgtattatt	gccagcagta	tgattctatt	300
ccttatacct	ttggccaggg	tacgaaagtt	gaaattaaac	gtacg		345

<210> 61

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 61

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tcgtgtacgg	gtactagcag	cgatgtgggc	ggctataact	atgtgagctg	gtaccagcag	120
catccccgga	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcggatc	caaaagcggc	aacaccgcga	gcctgaccat	tagcggcctg	240
caagcgggaag	acgaagcgga	ttattattgc	caggacgtgt	ttggcggcgg	cacgaagtta	300
accgttcttg	gccag					315

<210> 62

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 62

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tcgtgtacgg	gtactagcag	cgatgtgggc	ggctataact	atgtgagctg	gtaccagcag	120
catccccgga	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcggatc	caaaagcggc	aacaccgcga	gcctgaccat	tagcggcctg	240

caagcggaag acgaagcgga ttattattgc cagagctatg acatgtataa ttatattgtg 300  
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<210> 63  
 <211> 330  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VL domain

<400> 63  
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 catccccgga aggcgccgaa actgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg 180  
 agcaaccgtt ttagcggatc caaaagcggc aacaccgcga gcctgaccat tagcggcctg 240  
 caagcggaag acgaagcgga ttattattgc cagtctcatc atttttatga ggtgtttggc 300  
 ggcggcacga agttaaccgt tcttggccag 330

<210> 64  
 <211> 336  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VL domain

<400> 64  
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 catccccgga aggcgccgaa actgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg 180  
 agcaaccgtt ttagcggatc caaaagcggc aacaccgcga gcctgaccat tagcggcctg 240  
 caagcggaag acgaagcgga ttattattgc cagagctatg acaataattc tgatgttgtg 300  
 tttggcggcg gcacgaagtt aaccgttctt ggccag 336

<210> 65  
 <211> 306  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VL domain

<400> 65  
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 tcgtgtagcg gcgatgcgtt gggcgataaa tacgcgagct ggtaccagca gaaaccggg 120  
 caggcgccag ttctgggtgat ttatgatgat tctgaccgtc cctcaggcat cccggaacgc 180  
 tttagcggat ccaacagcgg caaacaccgc accctgacca ttagcggcac tcaggcggaa 240  
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 ggccag 306

<210> 66  
 <211> 324  
 <212> DNA  
 <213> Artificial Sequence

<220>



<223> polynucleotide sequence of a VL domain

<400> 66

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caggcgccag	ttctggtgat	ttatgatgat	tctgaccgtc	cctcaggcat	cccggaacgc	180
tttagcggat	ccaacagcgg	caacaccgcg	accctgacca	ttagcggcac	tcaggcggaa	240
gacgaagcgg	attattattg	ccagagctat	gactatttta	agcttgtgtt	tggcggcggc	300
acgaagttaa	ccgttcttgg	ccag				324

<210> 67

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 67

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tcgtgtagcg	gcatgacgct	gggcgataaa	tacgcgagct	ggtaccagca	gaaacccggg	120
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tttagcggat	ccaacagcgg	caacaccgcg	accctgacca	ttagcggcac	tcaggcggaa	240
gacgaagcgg	attattattg	ccagagctat	gactattctg	ctgattatgt	gtttggcggc	300
ggcacgaagt	taaccgttct	tggccag				327

<210> 68

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 68

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tttagcggat	ccaacagcgg	caacaccgcg	accctgacca	ttagcggcac	tcaggcggaa	240
gacgaagcgg	attattattg	ccagagctat	gactttgatt	ttgctgtgtt	tggcggcggc	300
acgaagttaa	ccgttcttgg	ccag				324

<210> 69

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 69

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caggcgccag	ttctggtgat	ttatgatgat	tctgaccgtc	cctcaggcat	cccggaacgc	180
tttagcggat	ccaacagcgg	caacaccgcg	accctgacca	ttagcggcac	tcaggcggaa	240
gacgaagcgg	attattattg	ccagagctat	gacggctcctg	atctttgggt	gtttggcggc	300
ggcacgaagt	taaccgttct	tggccag				327

<210> 70  
 <211> 332  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VH domain

<220>  
 <221> misc\_feature  
 <222> (1)..(3)  
 <223> NNN=GAA OR CAG

<400> 70  
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 cctgggcagg gtctcgagt gatgggcggc attattccga tttttggcac ggcgaactac 180  
 gcgcagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240  
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 ggccaaggca ccctggtgac ggtagctca gc 332

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 <211> 359  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VH domain

<400> 71  
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 cctgggcagg gtctcgagt gatgggcggc attattccga tttttggcac ggcgaactac 180  
 gcgcagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240  
 atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtgataat 300  
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<210> 72  
 <211> 359  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VH domain

<400> 72  
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 agctgcaaag cctccggagg cacttttagc agctatgcga ttagctgggt gcgccaagcc 120  
 cctgggcagg gtctcgagt gatgggcggc attattccga tttttggcac ggcgaactac 180  
 gcgcagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240  
 atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtgttaat 300  
 cattggactt atacttttga ttattggggc caaggcaccc tggtgacggt tagctcagc 359

<210> 73  
 <211> 374  
 <212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 73

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agctgcaaag	cctccggagg	cacttttagc	agctatgcga	ttagctgggt	gcgccaagcc	120
cctgggcagg	gtctcgagt	gatgggcggc	attattccga	tttttggcac	ggcgaactac	180
gcgcagaagt	ttcagggccg	ggtgaccatt	accgcggatg	aaagcaccag	caccgcgtat	240
atggaactga	gcagcctgcg	tagcgaagat	acggccgtgt	attattgcgc	gcgtgggtgt	300
ggttgggttt	ctcatggtta	ttattatctt	tttgatcttt	ggggccaagg	caccctgggtg	360
acggttagct	cagc					374

<210> 74

<211> 332

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<220>

<221> misc\_feature

<222> (1)..(3)

<223> NNN=GAA OR CAG

<400> 74

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cctgggcagg	gtctcgagt	gatgggctgg	attaaccgga	atagcggcgg	cacgaactac	180
gcgcagaagt	ttcagggccg	ggtgaccatg	acccgtgata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctgcg	tagcgaagat	acggccgtgt	attattgcgc	gcgtgattgg	300
ggccaaggca	ccctggtgac	ggttagctca	gc			332

<210> 75

<211> 380

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 75

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agctgcaaag	cctccggata	tacctttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctgggcagg	gtctcgagt	gatgggctgg	attaaccgga	atagcggcgg	cacgaactac	180
gcgcagaagt	ttcagggccg	ggtgaccatg	acccgtgata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctgcg	tagcgaagat	acggccgtgt	attattgcgc	gcgtaatatg	300
gcttatacta	attatcagta	tgtaatatg	cctcattttg	attattgggg	ccaaggcacc	360
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<210> 76

<211> 380

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; polynucleotide sequence of a VH domain

&lt;400&gt; 76

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agctgcaaag	cctccggata	tacctttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctgggcagg	gtctcgagt	gatgggctg	attaacccga	atagcggcg	cacgaactac	180
gcgcagaagt	ttcagggccg	ggtgaccat	acccgtgata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctgcg	tagcgaagat	acggccgtgt	attattgcgc	gcgttctatg	300
aattctacta	tgtattggt	tcttcgtcgt	gttctttttg	atcattgggg	ccaaggcacc	360
ctggtgacgg	ttagctcagc					380

&lt;210&gt; 77

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; polynucleotide sequence of a VH domain

&lt;400&gt; 77

caggtgcaat	tggttcagag	cggcgcgga	gtgaaaaaac	cggcgcgag	cgtgaaagt	60
agctgcaaag	cctccggata	tacctttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctgggcagg	gtctcgagt	gatgggctg	attaacccga	atagcggcg	cacgaactac	180
gcgcagaagt	ttcagggccg	ggtgaccat	acccgtgata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctgcg	tagcgaagat	acggccgtgt	attattgcgc	gcgtgatttt	300
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&lt;210&gt; 78

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; polynucleotide sequence of a VH domain

&lt;400&gt; 78

caggtgcaat	tggttcagag	cggcgcgga	gtgaaaaaac	cggcgcgag	cgtgaaagt	60
agctgcaaag	cctccggata	tacctttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctgggcagg	gtctcgagt	gatgggctg	attaacccga	atagcggcg	cacgaactac	180
gcgcagaagt	ttcagggccg	ggtgaccat	acccgtgata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctgcg	tagcgaagat	acggccgtgt	attattgcgc	gcgttattat	300
ggttcttctc	tttatcatta	tgtttttgg	ggtttttatt	attattgggg	ccaaggcacc	360
ctggtgacgg	ttagctcagc					380

&lt;210&gt; 79

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; polynucleotide sequence of a VH domain

&lt;400&gt; 79

caggtgcaat	tggttcagag	cggcgcgga	gtgaaaaaac	cggcgcgag	cgtgaaagt	60
agctgcaaag	cctccggata	tacctttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctgggcagg	gtctcgagt	gatgggctg	attaacccga	atagcggcg	cacgaactac	180
gcgcagaagt	ttcagggccg	ggtgaccat	acccgtgata	ccagcattag	caccgcgtat	240

## 81408-4400.ST25.txt

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atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcg gcgtgggttat 300
tggtatgctt attttactta tattaattat gggtattttg ataattgggg ccaaggcacc 360
ctggtgacgg ttagctcagc                                     380

```

```

<210> 80
<211> 383
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> polynucleotide sequence of a VH domain

```

```

<400> 80
caggtgcaat tggttcagag cggcgcgga gtgaaaaaac cgggcgcgag cgtgaaagtg 60
agctgcaaag cctccggata tacctttacc agctattata tgcactgggt ccgccaagcc 120
cctgggcagg gtctcgagt gatgggctgg attaaccga atagcggcg caggaactac 180
gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240
atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcg gcgtacttgg 300
cagtattctt atttttatta tcttgatggt gggtattatt ttgatatttg gggccaaggg 360
accctggtga cggttagctc agc                                     383

```

```

<210> 81
<211> 335
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> polynucleotide sequence of a VH domain

```

```

<220>
<221> misc_feature
<222> (1)..(3)
<223> NNN=GAA OR CAG

```

```

<400> 81
nnngtgcaat tgaaagaaag cggcccggcc ctggtgaaac cgacccaaac cctgaccctg 60
acctgtacct tttccggatt tagcctgtcc acgtctggcg ttggcgtggg ctggattcgc 120
cagccgcctg ggaaagccct cgagtggctg gctctgattg attgggatga tgataagtat 180
tatagcacca gcctgaaaac gcgtctgacc attagcaaag atacttcgaa aaatcaggtg 240
gtgctgacta tgaccaacat ggaccgggtg gatacggcc cctattattg cgcgcggtgat 300
tggggccaag gcaccctggt gacggttagc tcagc                                     335

```

```

<210> 82
<211> 392
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> polynucleotide sequence of a VH domain

```

```

<400> 82
caggtgcaat tgaaagaaag cggcccggcc ctggtgaaac cgacccaaac cctgaccctg 60
acctgtacct tttccggatt tagcctgtcc acgtctggcg ttggcgtggg ctggattcgc 120
cagccgcctg ggaaagccct cgagtggctg gctctgattg attgggatga tgataagtat 180
tatagcacca gcctgaaaac gcgtctgacc attagcaaag atacttcgaa aaatcaggtg 240
gtgctgacta tgaccaacat ggaccgggtg gatacggcc cctattattg cgcgcggttat 300
cattcttggt atgagatggg ttattatggt tctactgttg gttatatgtt tgattattgg 360

```

ggccaaggca ccctggtgac ggtagctca gc

392

<210> 83  
 <211> 341  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VH domain

<220>  
 <221> misc\_feature  
 <222> (1)..(3)  
 <223> NNN=GAA OR CAG

<400> 83  
 nnngtgcaat tgcaacagtc tgggtccgggc ctggtgaaac cgagccaaac cctgagcctg 60  
 acctgtgcga tttccggaga tagcgtgagc agcaacagcg cggcgtggaa ctggattcgc 120  
 cagtctcctg ggcgtggcct cgagtggctg ggccgtacct attatcgtag caaatggtat 180  
 aacgattatg cgtgagcgt gaaaagccgg attaccatca acccggtac ttcgaaaaac 240  
 cagtttagcc tgcaactgaa cagcgtgacc ccggaagata cggccgtgta ttattgcgcg 300  
 cgtgattggg gccaaggcac cctggtgacg gttagctcag c 341

<210> 84  
 <211> 362  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> polynucleotide sequence of a VH domain

<400> 84  
 caggtgcaat tgcaacagtc tgggtccgggc ctggtgaaac cgagccaaac cctgagcctg 60  
 acctgtgcga tttccggaga tagcgtgagc agcaacagcg cggcgtggaa ctggattcgc 120  
 cagtctcctg ggcgtggcct cgagtggctg ggccgtacct attatcgtag caaatggtat 180  
 aacgattatg cgtgagcgt gaaaagccgg attaccatca acccggtac ttcgaaaaac 240  
 cagtttagcc tgcaactgaa cagcgtgacc ccggaagata cggccgtgta ttattgcgcg 300  
 cgttcttatt atcctgattt tgattattgg ggccaaggca ccctggtgac ggtagctca 360  
 gc 362

<210> 85  
 <211> 109  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> polypeptide sequence of a VL domain

<400> 85

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln  
 1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala  
 20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr

```

          35              40              45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50              55              60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65              70              75              80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Ser Ala Asp Tyr
          85              90              95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
          100              105

```

```

<210> 86
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 86

```

```

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1              5              10              15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
          20              25              30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
          35              40              45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
          50              55              60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65              70              75              80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser His His Phe Tyr
          85              90              95

Glu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
          100              105              110

```

```

<210> 87
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 87

```

```

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1              5              10              15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala

```

```

                20                25                30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
   35                40                45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
   50                55                60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
   65                70                75                80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Asp Phe Ala Val
           85                90                95
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
   100                105

```

```

<210> 88
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 88

```

```

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1           5           10           15
Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
           20           25           30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
           35           40           45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
           50           55           60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65           70           75           80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
           85           90           95
Tyr Asp Ser Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
           100          105          110
Lys Arg Thr
           115

```

```

<210> 89
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

```



&lt;400&gt; 89

```

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
          20           25           30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
          35           40           45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
          50           55           60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65           70           75           80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Met Ser Asn Tyr Pro
          85           90           95
Asp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
          100          105          110

```

&lt;210&gt; 90

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; polypeptide sequence of a VL domain

&lt;400&gt; 90

```

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1           5           10           15
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
          20           25           30
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
          35           40           45
Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
          50           55           60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65           70           75           80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asn Asn
          85           90           95
Ser Asp Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
          100          105          110

```

&lt;210&gt; 91

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; polypeptide sequence of a VL domain

&lt;400&gt; 91

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Phe Gln Tyr Gly Ser Ile Pro Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr  
 100 105

&lt;210&gt; 92

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; polypeptide sequence of a VL domain

&lt;400&gt; 92

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Asn Ala Pro  
 85 90 95

Val Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr  
 100 105 110

&lt;210&gt; 93

&lt;211&gt; 108

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> polypeptide sequence of a VL domain

<400> 93

```

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1           5           10           15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
          20           25           30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
          35           40           45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
          50           55           60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65           70           75           80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Phe Lys Leu Val
          85           90           95
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
          100           105

```

<210> 94  
 <211> 112  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> polypeptide sequence of a VL domain

<400> 94

```

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1           5           10           15
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
          20           25           30
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
          35           40           45
Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
          50           55           60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65           70           75           80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Tyr
          85           90           95
Asn Tyr Ile Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
          100           105           110

```

<210> 95  
 <211> 109  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> polypeptide sequence of a VL domain

<400> 95

```

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1           5           10           15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
          20           25           30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
          35           40           45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
          50           55           60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65           70           75           80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gly Pro Asp Leu Trp
          85           90           95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
          100          105

```

<210> 96  
 <211> 118  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> polypeptide sequence of a VH domain

<400> 96

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
          20           25           30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35           40           45
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
          50           55           60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65           70           75           80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85           90           95

```

Ala Arg Asp Phe Leu Gly Tyr Glu Phe Asp Tyr Trp Gly Gln Gly Thr  
                   100                                  105                                  110

Leu Val Thr Val Ser Ser  
                   115

<210> 97  
 <211> 126  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> polypeptide sequence of a VH domain

<400> 97

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
   1                                  5                                  10                                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
                   20                                  25                                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
                   35                                  40                                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe  
                   50                                  55                                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
   65                                  70                                  75                                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                  90                                  95

Ala Arg Tyr Tyr Gly Ser Ser Leu Tyr His Tyr Val Phe Gly Gly Phe  
                   100                                  105                                  110

Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
                   115                                  120                                  125

<210> 98  
 <211> 130  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> polypeptide sequence of a VH domain

<400> 98

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
   1                                  5                                  10                                  15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
                   20                                  25                                  30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
                   35                                  40                                  45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser  
 50 55 60  
 Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
 65 70 75 80  
 Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
 85 90 95  
 Cys Ala Arg Tyr His Ser Trp Tyr Glu Met Gly Tyr Tyr Gly Ser Thr  
 100 105 110  
 Val Gly Tyr Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val  
 115 120 125  
 Ser Ser  
 130

<210> 99  
 <211> 119  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> polypeptide sequence of a VH domain  
 <400> 99

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr  
 20 25 30  
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45  
 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe  
 50 55 60  
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Asp Asn Trp Phe Lys Pro Phe Ser Asp Val Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> 100  
 <211> 119  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> polypeptide sequence of a VH domain

&lt;400&gt; 100

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr  
 20 25 30  
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45  
 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe  
 50 55 60  
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Val Asn His Trp Thr Tyr Thr Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

&lt;210&gt; 101

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; polypeptide sequence of a VH domain

&lt;400&gt; 101

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 20 25 30  
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45  
 Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe  
 50 55 60  
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Gly Tyr Trp Tyr Ala Tyr Phe Thr Tyr Ile Asn Tyr Gly Tyr  
 100 105 110  
 Phe Asp Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120 125

<210> 102  
 <211> 124  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> polypeptide sequence of a VH domain

<400> 102

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
          20          25          30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50          55          60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65          70          75          80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Arg Gly Gly Gly Trp Val Ser His Gly Tyr Tyr Tyr Leu Phe Asp
          100          105          110
Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
          115          120

```

<210> 103  
 <211> 127  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> polypeptide sequence of a VH domain

<400> 103

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
          20          25          30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
          50          55          60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65          70          75          80

```



Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
                             85                            90                            95

Ala Arg Thr Trp Gln Tyr Ser Tyr Phe Tyr Tyr Leu Asp Gly Gly Tyr  
                             100                            105                            110

Tyr Phe Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
                             115                            120                            125

<210> 104

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VH domain

<400> 104

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
  1                            5                            10                            15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
                             20                            25                            30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
                             35                            40                            45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe  
                             50                            55                            60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
  65                            70                            75                            80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
                             85                            90                            95

Ala Arg Asn Met Ala Tyr Thr Asn Tyr Gln Tyr Val Asn Met Pro His  
                             100                            105                            110

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
                             115                            120                            125

<210> 105

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VH domain

<400> 105

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
  1                            5                            10                            15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
                             20                            25                            30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
           35                          40                          45  
 Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe  
           50                          55                          60  
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
           65                          70                          75                          80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
                           85                          90                          95  
 Ala Arg Ser Met Asn Ser Thr Met Tyr Trp Tyr Leu Arg Arg Val Leu  
                           100                          105                          110  
 Phe Asp His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
           115                          120                          125

<210> 106  
 <211> 120  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> polypeptide sequence of a VH domain  
  
 <400> 106

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1                          5                          10                          15  
 Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn  
           20                          25                          30  
 Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu  
           35                          40                          45  
 Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
           50                          55                          60  
 Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn  
           65                          70                          75                          80  
 Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val  
                           85                          90                          95  
 Tyr Tyr Cys Ala Arg Ser Tyr Tyr Pro Asp Phe Asp Tyr Trp Gly Gln  
           100                          105                          110  
 Gly Thr Leu Val Thr Val Ser Ser  
           115                          120